AMENDMENTS TO THE CLAIMS

1-53. Canceled

54. (Currently amended) ~~The method of claim 42,~~ A method for predicting a human breast cancer patient as having a good prognosis or a poor prognosis, comprising:

    (a)   classifying said breast cancer patient into one of the following classes:

        (a1) ER⁻ and sporadic;

        (a2) ER⁻ and *BRCA1*;

        (a3) ER+ and ER/AGE high;

        (a4) ER+, ER/AGE low and LN+; or

        (a5) ER+, ER/AGE low and LN⁻;

wherein ER^+ designates a high ER level and ER⁻ designates a low ER level, wherein said ER/AGE is a metric of said ER level relative to the age of said patient, and wherein LN^+ designates a greater than 0 lymph nodes status in said patient and LN⁻ designates a 0 lymph nodes status in said patient, and wherein said ER/AGE is classified as high if said ER level is greater than $c \cdot (AGE - d)$, and wherein said ER/AGE is classified as low if said ER level is equal to or less than $c \cdot (AGE - d)$, wherein c is a coefficient, AGE is the age of said patient, and d is an age threshold;

    (b)   determining a profile comprising measurements of levels of transcripts of, or proteins encoded by, respective genes in a plurality of genes in a cell sample taken from said breast cancer patient, said respective genes comprising:

        (b1)   at least five of the genes for which markers are listed in Table 1 if said breast cancer patient is classified as ER⁻ and sporadic;

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(b2)   at least two of the genes for which markers are listed in Table 2 if said breast cancer patient is classified as ER⁻ and *BRCA1*;

(b3)   at least two of the genes for which markers are listed in Table 3 if said breast cancer patient is classified as ER+ and ER/AGE high;

(b4)   at least two of the genes for which markers are listed in Table 4 if said breast cancer patient is classified as ER+, ER/AGE low and LN+; or

(b5)   at least two of the genes for which markers are listed in Table 5 if said breast cancer patient is classified as ER+, ER/AGE low and LN⁻; and

(c)   comparing, on a computer, said profile to a good prognosis template and/or a poor prognosis template, wherein said good prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes a plurality of good outcome patients, and said poor prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of poor outcome patients, and wherein a good outcome patient is a breast cancer patient who has non-reoccurrence of metastases within a first period of time after initial diagnosis and a poor outcome patient is a patient who has reoccurrence of metastases within a second period of time after initial diagnosis; and

(d)   classifying said breast cancer patient (i) as having a good prognosis if said profile has a high similarity to said good prognosis template, has a low similarity to said poor prognosis template, or has a higher similarity to said good prognosis template than to said poor prognosis template, wherein said profile has a high similarity to said good prognosis template if the similarity to said good prognosis template is above a predetermined threshold, or has a low similarity to said poor prognosis template if the similarity to said poor prognosis template is below said predetermined threshold, or (ii) as having a poor prognosis if said profile has a high

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similarity to said poor prognosis template, has a low similarity to said good prognosis template, or has a higher similarity to said poor prognosis template than to said good prognosis template, wherein said profile has a high similarity to said poor prognosis template if the similarity to said poor prognosis template is above said predetermined threshold, or has a low similarity to said good prognosis template if the similarity to said good prognosis template is below said predetermined threshold.

55-57. (Canceled)

58.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and sporadic, and said plurality of genes comprises at least [[two]] ten of the genes for which markers are listed in Table 1.

59.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and sporadic, and said plurality of genes comprises all of the genes for which markers are listed in Table 1.

60.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and *BRCA1*, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 2.

61.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and *BRCA1*, and said plurality of genes comprises all of the genes for which markers are listed in Table 2

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62.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+ and ER/AGE high, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 3.

63.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+ and ER/AGE high, and said plurality of genes comprises all of the genes for which markers are listed in Table 3.

64.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN+, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 4.

65.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN+, and said plurality of genes comprises all of the genes for which markers are listed in Table 4.

66.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN⁻, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 5.

67.   (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN⁻, and said plurality of genes comprises all of the genes for which markers are listed in Table 5.

68-93. (Canceled)

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94.   (Currently amended) ~~The method of claim 89,~~ A computer-implemented method for predicting a human breast cancer patient as having a good prognosis or a poor prognosis, comprising:

(a) classifying, on a computer, said patient as having a good prognosis or a poor prognosis based on a profile comprising measurements of levels of transcripts of, or proteins encoded by, respective genes in a plurality of genes in a cell sample taken from said patient, said plurality of genes comprising:

(b1)   at least five of the genes for which markers are listed in Table 1 if said patient is ER⁻ and sporadic;

(b2)   at least two of the genes for which markers are listed in Table 2 if said patient is ER⁻ and *BRCA1*;

(b3)   at least two of the genes for which markers are listed in Table 3 if said patient is ER+ and ER/AGE high;

(b4)   at least two of the genes for which markers are listed in Table 4 if said patient is ER+, ER/AGE low and LN+; or

(b5)   at least two of the genes for which markers are listed in Table 5 if said patient is ER+, ER/AGE low and LN⁻,

wherein ER^+ designates a high ER level and ER^- designates a low ER level, wherein said ER/AGE is a metric of said ER level relative to the age of said patient, wherein LN^+ designates a greater than 0 lymph nodes status in said patient and LN^- designates a 0 lymph nodes status in patient, and wherein said ER/AGE is classified as high if said ER level is greater than $c \cdot (AGE - d)$, and wherein said ER/AGE is classified as low if said ER level is equal to or less than $c \cdot (AGE - d)$, wherein c is a coefficient, AGE is the age of said patient, and d is an age threshold,

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wherein said classifying is carried out by a method comprising comparing said profile to a good prognosis template and/or a poor prognosis template, wherein said good prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of good outcome patients, and said poor prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of poor outcome patients, and wherein a good outcome patient is a breast cancer patient who has non-reoccurrence of metastases within a first period of time after initial diagnosis and a poor outcome patient is a breast cancer patient who has reoccurrence of metastases within a second period of time after initial diagnosis, and wherein:

(i) said individual is classified as having a good prognosis if said profile has a high similarity to said good prognosis template, has a low similarity to said poor prognosis template, or has a higher similarity to said good prognosis template than to said poor prognosis template, wherein said profile has a high similarity to said good prognosis template if the similarity to said good prognosis template is above a predetermined threshold, or has a low similarity to said poor prognosis template if the similarity to said poor prognosis template is below said predetermined threshold, or

(ii) said individual is classified as having a poor prognosis if said profile has a high similarity to said poor prognosis template, has a low similarity to said good prognosis template, or has a higher similarity to said poor prognosis template than to said good prognosis template, wherein said profile has a high similarity to said poor prognosis template if the similarity to said poor prognosis template is above said predetermined threshold, or has a low similarity to said good prognosis template if the similarity to said good prognosis template is below said predetermined threshold.

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95.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER⁻ and sporadic, and said plurality of genes comprises at least ten two of the genes for which markers are listed in Table 1.

96.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER⁻ and sporadic, and said plurality of genes comprises all of the genes for which markers are listed in Table 1.

97.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER⁻ and *BRCA1*, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 2.

98.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER⁻ and *BRCA1*, and said plurality of genes comprises all of the genes for which markers are listed in Table 2.

99.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+ and ER/AGE high, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 3.

100.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+ and ER/AGE high, and said plurality of genes comprises all of the genes for which markers are listed in Table 3.

101.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+; ER/AGE low and LN+, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 4.

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102.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN+, and said plurality of genes comprises all of the genes for which markers are listed in Table 4.

103.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN−, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 5.

104.   (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN−, and said plurality of genes comprises all of the genes for which markers are listed in Table 5.

105.   (Canceled)

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